

502

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10|521,513  
Source: PCT  
Date Processed by STIC: 01|10|2006

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 01/10/2006

PATENT APPLICATION: US/10/521,513

TIME: 08:14:46

Input Set : N:\CrF3\RULE60\10521513.raw.txt

Output Set: N:\CRF4\01102006\J521513.raw

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1 <110> APPLICANT: BIOGEN, INC.
2 <120> TITLE OF INVENTION: THERAPIES FOR RENAL FAILURE USING INTERFERON-BETA
3 <130> FILE REFERENCE: BII-001.25
4 <140> CURRENT APPLICATION NUMBER: US 10/521,513
5 <141> CURRENT FILING DATE: 2005-01-18
6 <150> PRIOR APPLICATION NUMBER: PCT/US03/22440
7 <151> PRIOR FILING DATE: 2003-07-17
8 <150> PRIOR APPLICATION NUMBER: US 60/396,393
9 <151> PRIOR FILING DATE: 2002-07-17
10 <160> NUMBER OF SEQ ID NOS: 21
11 <170> SOFTWARE: PatentIn Ver. 2.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 840
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
17 <220> FEATURE:
18 <221> NAME/KEY: CDS
19 <222> LOCATION: (76)..(636)
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21      acattctaac tgcaaccttt cgaagccttt gctctggcac aacaggtagt aggcgacact 60
22      gttcgtgttg tcaac atg acc aac aag tgt ctc ctc caa att gct ctc ctg 111
23                      Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu
24                      1          5          10
25      ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga 159
26      Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly
27                      15          20          25
28      ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa 207
29      Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln
30      30          35          40
31      ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac 255
32      Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp
33      45          50          55          60
34      atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc 303
35      Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
36      65          70          75
37      gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga 351
38      Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg
39      80          85          90
40      caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc 399
41      Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
42      95          100          105
43      ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa 447
44      Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu

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Input Set : N:\CrF3\RULE60\10521513.raw.txt

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45          110          115          120
46    gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt    495
47    Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser
48    125          130          135          140
49    ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc    543
50    Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
51          145          150          155
52    aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta    591
53    Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
54          160          165          170
55    agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac    636
56    Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
57    175          180          185
58    tgaagatctc ctagcctgtg cctctgggac tggacaattg cttcaagcat tcttcaacca    696
59    gcagatgctg ttttaagtgc tgatggctaa tgtactgcat atgaaaggac actagaagat    756
60    tttgaaattt ttattaaatt atgagttatt tttattttat taaattttat tttggaaaat    816
61    aaattatttt tggtgcaaaa gtca    840
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 187
65 <212> TYPE: PRT
66 <213> ORGANISM: Homo sapiens
67 <400> SEQUENCE: 2
68    Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
69    1          5          10          15
70    Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
71          20          25          30
72    Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
73          35          40          45
74    Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
75          50          55          60
76    Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
77          65          70          75          80
78    Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
79          85          90          95
80    Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
81          100          105          110
82    Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
83          115          120          125
84    Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
85          130          135          140
86    Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
87          145          150          155          160
88    His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
89          165          170          175
90    Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
91          180          185
93 <210> SEQ ID NO: 3
94 <211> LENGTH: 501
95 <212> TYPE: DNA

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Input Set : N:\CrF3\RULE60\10521513.raw.txt

Output Set: N:\CRF4\01102006\J521513.raw

96 &lt;213&gt; ORGANISM: Homo sapiens

97 &lt;220&gt; FEATURE:

98 &lt;221&gt; NAME/KEY: CDS

99 &lt;222&gt; LOCATION: (1)..(498)

100 &lt;400&gt; SEQUENCE: 3

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101      atg agc tac aac ttg ctt gga ttc cta caa aga agc agc aat ttt cag      48
102      Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
103      1              5              10              15
104      tgt cag aag ctc ctg tgg caa ttg aat ggg agg ctt gaa tac tgc ctc      96
105      Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
106      20              25              30
107      aag gac agg atg aac ttt gac atc cct gag gag att aag cag ctg cag      144
108      Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
109      35              40              45
110      cag ttc cag aag gag gac gcc gca ttg acc atc tat gag atg ctc cag      192
111      Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
112      50              55              60
113      aac atc ttt gct att ttc aga caa gat tca tct agc act ggc tgg aat      240
114      Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
115      65              70              75              80
116      gag act att gtt gag aac ctc ctg gct aat gtc tat cat cag ata aac      288
117      Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
118      85              90              95
119      cat ctg aag aca gtc ctg gaa gaa aaa ctg gag aaa gaa gat ttc acc      336
120      His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
121      100             105             110
122      agg gga aaa ctc atg agc agt ctg cac ctg aaa aga tat tat ggg agg      384
123      Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
124      115             120             125
125      att ctg cat tac ctg aag gcc aag gag tac agt cac tgt gcc tgg acc      432
126      Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
127      130             135             140
128      ata gtc aga gtg gaa atc cta agg aac ttt tac ttc att aac aga ctt      480
129      Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
130      145             150             155             160
131      aca ggt tac ctc cga aac tga      501
132      Thr Gly Tyr Leu Arg Asn
133      165

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135 &lt;210&gt; SEQ ID NO: 4

136 &lt;211&gt; LENGTH: 166

137 &lt;212&gt; TYPE: PRT

138 &lt;213&gt; ORGANISM: Homo sapiens

139 &lt;400&gt; SEQUENCE: 4

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140      Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
141      1              5              10              15
142      Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
143      20              25              30
144      Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
145      35              40              45

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## RAW SEQUENCE LISTING

DATE: 01/10/2006

PATENT APPLICATION: US/10/521,513

TIME: 08:14:46

Input Set : N:\Crif3\RULE60\10521513.raw.txt

Output Set: N:\CRF4\01102006\J521513.raw

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146      Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
147          50                      55                      60
148      Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
149          65                      70                      75                      80
150      Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
151          85                      90                      95
152      His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
153          100                    105                    110
154      Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
155          115                    120                    125
156      Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
157          130                    135                    140
158      Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
159          145                    150                    155                    160
160      Thr Gly Tyr Leu Arg Asn
161          165
163 <210> SEQ ID NO: 5
164 <211> LENGTH: 15
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker
169      oligonucleotide
170 <400> SEQUENCE: 5
171      ggcggtggtg gcagc
172                                     15
173 <210> SEQ ID NO: 6
174 <211> LENGTH: 5
175 <212> TYPE: PRT
176 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker peptide
179 <400> SEQUENCE: 6
180      Gly Gly Gly Gly Ser
181          1                      5
183 <210> SEQ ID NO: 7
184 <211> LENGTH: 15
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence: Enterokinase
189      recognition site oligonucleotide
190 <400> SEQUENCE: 7
191      gacgatgatg acaag
192                                     15
193 <210> SEQ ID NO: 8
194 <211> LENGTH: 5
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence: Enterokinase

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Input Set : N:\Crf3\RULE60\10521513.raw.txt

Output Set: N:\CRF4\01102006\J521513.raw

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199      recognition site
200 <400> SEQUENCE: 8
201      Asp Asp Asp Asp Lys
202      1          5
204 <210> SEQ ID NO: 9
205 <211> LENGTH: 24
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Description of Artificial Sequence: Modified enterokinase
210      recognition site oligonucleotide
211 <400> SEQUENCE: 9
212      agctccggag acgatgatga caag
214 <210> SEQ ID NO: 10
215 <211> LENGTH: 8
216 <212> TYPE: PRT
217 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence: Modified
220      enterokinase recognition site
221 <400> SEQUENCE: 10
222      Ser Ser Gly Asp Asp Asp Lys
223      1          5
225 <210> SEQ ID NO: 11
226 <211> LENGTH: 1257
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <221> NAME/KEY: CDS
231 <222> LOCATION: (1)..(1254)
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
234      IFN-beta G162C-Ig direct fusion construct nucleotide
235      sequence
236 <400> SEQUENCE: 11
237      atg cct ggg aag atg gtc gtg atc ctt gga gcc tca aat ata ctt tgg
238      Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
239      1          5          10          15
240      ata atg ttt gca gct tct caa gcc atg agc tac aac ttg ctt gga ttc
241      Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Gly Phe
242      20          25          30
243      cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa ttg
244      Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu
245      35          40          45
246      aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac atc
247      Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile
248      50          55          60
249      cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc gca
250      Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 01/10/2006  
PATENT APPLICATION:    US/10/521,513      TIME: 08:14:47

Input Set : N:\Crf3\RULE60\10521513.raw.txt  
Output Set: N:\CRF4\01102006\J521513.raw

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The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 209

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/521,513

DATE: 01/10/2006

TIME: 08:14:47

Input Set : N:\Crf3\RULE60\10521513.raw.txt

Output Set: N:\CRF4\01102006\J521513.raw



**STATISTICS SUMMARY**

PATENT APPLICATION: US/10/521,513

DATE: 01/10/2006

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Input Set : N:\Crf3\RULE60\10521513.raw.txt

Output Set: N:\CRF4\01102006\J521513.raw

Application Serial Number: US/10/521,513

Alpha or Numeric or Xml: Numeric

Application Class:

Application File Date: 01-18-2005

Art Unit: PCT

Software Application: PatentIN2.1

Total Number of Sequences: 21

Total Nucleotides: 4020

Total Amino Acids: 1252

Number of Errors: 0

Number of Warnings: 0

Number of Corrections: 0

**MESSAGE SUMMARY**